



OIPF

RAW SEQUENCE LISTING

DATE: 11/21/2002

PATENT APPLICATION: US/09/902,481B

TIME: 10:19:18

Input Set : A:\A70586-1 Proposed Substitute.ST25.txt

Output Set: N:\CRF4\11212002\I902481B.raw

3 <110> APPLICANT: Springer, Timothy
 4 Shimaoka, Motomu
 5 Shifman, Julia
 6 Mayo, Stephen
 8 <120> TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
 10 <130> FILE REFERENCE: A-70586-1/RFT/RMS/RMK
 12 <140> CURRENT APPLICATION NUMBER: US 09/902,481B
 13 <141> CURRENT FILING DATE: 2001-07-09
 15 <150> PRIOR APPLICATION NUMBER: US 60/216,600
 16 <151> PRIOR FILING DATE: 2000-07-07
 18 <160> NUMBER OF SEQ ID NOS: 13
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1153
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 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: mat_peptide
 29 <222> LOCATION: (17)..()
 30 <223> OTHER INFORMATION:

p.6

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 39 1 5 10 15
 42 Gly Phe Gly Gln Ser Val Val Gln Leu Gln Gly Ser Arg Val Val Val
 43 20 25 30
 46 Gly Ala Pro Gln Glu Ile Val Ala Ala Asn Gln Arg Gly Ser Leu Tyr
 47 35 40 45
 50 Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val
 51 50 55 60
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 55 65 70 75 80
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 59 85 90 95
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 63 100 105 110
 66 Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys
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 71 130 135 140
 74 Ile Ile Pro His Asp Phe Arg Arg Met Lys Glu Phe Val Ser Thr Val
 75 145 150 155 160

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82 Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn
83          180          185          190
86 Pro Asn Pro Arg Ser Leu Val Lys Pro Ile Thr Gln Leu Leu Gly Arg
87          195          200          205
90 Thr His Thr Ala Thr Gly Ile Arg Lys Val Val Arg Glu Leu Phe Asn
91          210          215          220
94 Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Val Val Ile
95 225          230          235          240
98 Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile
99          245          250          255
102 Pro Glu Ala Asp Arg Glu Gly Val Ile Arg Tyr Val Ile Gly Val Gly
103          260          265          270
106 Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Ile Ala
107          275          280          285
110 Ser Lys Pro Pro Arg Asp His Val Phe Gln Val Asn Asn Phe Glu Ala
111          290          295          300
114 Leu Lys Thr Ile Gln Asn Gln Leu Arg Glu Lys Ile Phe Ala Ile Glu
115 305          310          315          320
118 Gly Thr Gln Thr Gly Ser Ser Ser Ser Phe Glu His Glu Met Ser Gln
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122 Glu Gly Phe Ser Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr
123          340          345          350
126 Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys
127          355          360          365
130 Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn
131          370          375          380
134 Asp Ala Tyr Leu Gly Tyr Ala Ala Ala Ile Ile Leu Arg Asn Arg Val
135 385          390          395          400
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139          405          410          415
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154 His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu
155 465          470          475          480
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159          485          490          495
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163          500          505          510
166 Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro
167          515          520          525
170 Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser
171          530          535          540
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183          580          585          590
186 His Val Leu Leu Leu Arg Ser Gln Pro Val Leu Arg Val Lys Ala Ile
187          595          600          605
190 Met Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn
191          610          615          620
194 Asp Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu
195 625          630          635          640
198 His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln
199          645          650          655
202 Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser
203          660          665          670
206 Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln
207          675          680          685
210 Val Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro
211          690          695          700
214 Asn Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe
215 705          710          715          720
218 Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val
219          725          730          735
222 Leu Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu
223          740          745          750
226 Lys Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr
227          755          760          765
230 Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu
231          770          775          780
234 Phe Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg
235 785          790          795          800
238 Thr Gln Val Thr Phe Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val
239          805          810          815
242 Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys
243          820          825          830
246 Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser
247          835          840          845
250 Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe
251          850          855          860
254 Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu
255 865          870          875          880
258 Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Met Pro Arg Thr Asn
259          885          890          895
262 Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met
263          900          905          910
266 Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala
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270 Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn
271          930          935          940

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274 Leu Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val
275 945          950          955          960
278 Arg Leu Asn Gln Thr Val Ile Trp Asp Arg Pro Gln Val Thr Phe Ser
279          965          970          975
282 Glu Asn Leu Ser Ser Thr Cys His Thr Lys Glu Arg Leu Pro Ser His
283          980          985          990
286 Ser Asp Phe Leu Ala Glu Leu Arg Lys Ala Pro Val Val Asn Cys Ser
287          995          1000          1005
290 Ile Ala Val Cys Gln Arg Ile Gln Cys Asp Ile Pro Phe Phe Gly
291          1010          1015          1020
294 Ile Gln Glu Glu Phe Asn Ala Thr Leu Lys Gly Asn Leu Ser Phe
295          1025          1030          1035
298 Asp Trp Tyr Ile Lys Thr Ser His Asn His Leu Leu Ile Val Ser
299          1040          1045          1050
302 Thr Ala Glu Ile Leu Phe Asn Asp Ser Val Phe Thr Leu Leu Pro
303          1055          1060          1065
306 Gly Gln Gly Ala Phe Val Arg Ser Gln Thr Glu Thr Lys Val Glu
307          1070          1075          1080
310 Pro Phe Glu Val Pro Asn Pro Leu Pro Leu Ile Val Gly Ser Ser
311          1085          1090          1095
314 Val Gly Gly Leu Leu Leu Leu Ala Leu Ile Thr Ala Ala Leu Tyr
315          1100          1105          1110
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336 ttcaacttgg aactgaaaa cgcaatgacc ttccaagaga acgcaagggg cttcggggcag      180
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396	ccagtactga	gagtcaaggc	aatcatggag	ttcaatccca	gggaagtggc	aaggaatgta	1980
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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